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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/974,973DATE: 05/30/2002
TIME: 09:24:49Input Set : A:\seqlist_1533 1230001.txt
Output Set: N:\CRF3\05302002\I974973.raw

5 <110> APPLICANT: Hanke, Paul D.
9 <120> TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from
Corynebacterium
13 <130> FILE REFERENCE: 1533.1230001/MAC/RGM
17 <140> CURRENT APPLICATION NUMBER: US 09/974,973
C--> 19 <141> CURRENT FILING DATE: 2001-10-21
23 <150> PRIOR APPLICATION NUMBER: US 60/239,913
25 <151> PRIOR FILING DATE: 2000-10-13
29 <160> NUMBER OF SEQ ID NOS: 19
33 <170> SOFTWARE: PatentIn version 3.0
37 <210> SEQ ID NO: 1
39 <211> LENGTH: 3474
41 <212> TYPE: DNA
43 <213> ORGANISM: Corynebacterium glutamicum
47 <220> FEATURE:
49 <221> NAME/KEY: CDS
51 <222> LOCATION: (1)..(3474)
55 <400> SEQUENCE: 1
56 gtg act atc acc ctt ggc ggt ctc ttg ttg aaa gga ata att act 48
57 Met Thr Ala Ile Thr Leu Gly Gly Leu Leu Lys Gly Ile Ile Thr
58 1 5 10 15
60 cta gtg tcg act cac aca tct tca acg ctt cca gca ttc aaa aag atc 96
61 Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
62 20 25 30
63 ttg gta gca aac cgc ggc gaa atc gcg gtc cgt gct ttc cgt gca gca 144
64 Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
65 35 40 45
67 ctc gaa acc ggt gca gcc acg gta gct att tac ccc cgt gaa gat cgg 192
68 Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg
69 50 55 60
71 gga tca ttc cac cgc tct ttt gct tct gaa gct gtc cgc att ggt act 240
72 Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
73 65 70 75 80
75 gaa ggc tca cca gtc aag gcg tac ctg gac atc gat gaa att atc ggt 288
76 Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
77 85 90 95
79 gca gct aaa aaa gtt aaa gca gat gct att tac ccg gga tat ggc ttc 336
80 Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
81 100 105 110
83 ctg tct gaa aat gcc cag ctt gcc cgc gag tgc gcg gaa aac ggc att 384
84 Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
85 115 120 125
87 act ttt att ggc cca acc cca gag gtt ctt gat ctc acc ggt gat aag 432
88 Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys

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89	130	135	140			
91	tct	cgt	gcf	gtc acc gcc gcg aag aag gct ggt ctg cca gtt ttg gcg	480	
92	Ser	Arg	Ala	Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala		
93	145		150	155	160	
95	gaa	tcc	acc	ccg agc aaa aac atc gat gac atc gtt aaa agc gct gaa	528	
96	Glu	Ser	Thr	Pro Ser Lys Asn Ile Asp Asp Ile Val Lys Ser Ala Glu		
97			165	170	175	
99	ggc	cag	act	tac ccc atc ttt gta aag gca gtt gcc ggt ggt ggc gga	576	
100	Gly	Gln	Thr	Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly		
101			180	185	190	
103	cgc	ggt	atg	cgc ttt gtt tct tca cct gat gag ctc cgc aaa ttg gca	624	
104	Arg	Gly	Met	Arg Phe Val Ser Ser Pro Asp Glu Leu Arg Lys Leu Ala		
105			195	200	205	
107	aca	gaa	gca	tct cgt gaa gct gaa gcg gca ttc ggc gac ggt tcg gta	672	
108	Thr	Glu	Ala	Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val		
109			210	215	220	
111	tat	gtc	gaa	cgt gct gtg att aac ccc cag cac att gaa gtg cag atc	720	
112	Tyr	Val	Glu	Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile		
113			225	230	235	240
115	ctt	ggc	gat	cgc act gga gaa gtt gta cac ctt tat gaa cgt gac tgc	768	
116	Leu	Gly	Asp	Arg Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys		
117			245	250	255	
119	tca	ctg	cag	cgt cac caa aaa gtt gtc gaa att gcg cca gca cag	816	
120	Ser	Leu	Gln	Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln		
121			260	265	270	
123	cat	ttg	gat	cca gaa ctg cgt gat cgc att tgt gcg gat gca gta aag	864	
124	His	Leu	Asp	Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys		
125			275	280	285	
127	ttc	tgc	ccg	tcc att ggt tac cag ggc gcg gga acc gtc gaa ttc ttg	912	
128	Phe	Cys	Arg	Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu		
129			290	295	300	
131	gtc	gat	gaa	aag ggc aac cac gtt ttc atc gaa atg aac cca cgt atc	960	
132	Val	Asp	Glu	Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile		
133			305	310	315	320
135	cag	gtt	gag	cac acc gtc act gaa gaa gtc acc gag gtc gac ctg gtg	1008	
136	Gln	Val	Glu	His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val		
137			325	330	335	
139	aag	gcf	cag	atg cgc ttg gct gct ggt gca acc ttg aag gaa ttg ggt	1056	
140	Lys	Ala	Gln	Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly		
141			340	345	350	
143	ctg	acc	caa	gat aag atc aag acc cac ggt gca gca ctg cag tgc cgc	1104	
144	Leu	Thr	Gln	Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg		
145			355	360	365	
147	atc	acc	acg	gaa gat cca aac aac ggc ttc cgc cca gat acc gga act	1152	
148	Ile	Thr	Thr	Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr		
149			370	375	380	
151	atc	acc	gcf	tac cgc tca cca ggc gga gct ggc gtt cgt ctt gac ggt	1200	
152	Ile	Thr	Ala	Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly		
153			385	390	395	400

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155	gca	gct	cag	ctc	ggg	ggc	gaa	atc	acc	gca	cac	ttt	gac	tcc	atg	ctg		1248
156	Ala	Ala	Gln	Leu	Gly	Gly	Glu	Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu		
157				405						410					415			
159	gtg	aaa	atg	acc	tgc	cgt	ggg	tcc	gac	ttt	gaa	act	gct	gtt	gct	cgt		1296
160	Val	Lys	Met	Thr	Cys	Arg	Gly	Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg		
161				420				425			430							
163	gca	cag	cgc	gcg	ttg	gct	gag	ttc	acc	gtg	tct	ggg	gtt	gca	acc	aac		1344
164	Ala	Gln	Arg	Ala	Leu	Ala	Glu	Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn		
165				435				440			445							
167	att	ggg	ttc	ttg	cgt	gcg	ttg	ctg	cgg	gaa	gag	gac	ttc	act	tcc	aag		1392
168	Ile	Gly	Phe	Leu	Arg	Ala	Leu	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ser	Lys		
169				450				455			460							
171	cgc	atc	gcc	acc	gga	ttt	atc	ggc	gat	cac	cca	cac	ctc	ttt	cag	gct		1440
172	Arg	Ile	Ala	Thr	Gly	Phe	Ile	Gly	Asp	His	Pro	His	Leu	Leu	Gln	Ala		
173	465				470					475			480					
175	cca	cct	gcg	gat	gat	gag	cag	gga	cgc	atc	ctg	gat	tac	ttg	gca	gat		1488
176	Pro	Pro	Ala	Asp	Asp	Glu	Gln	Gly	Arg	Ile	Leu	Asp	Tyr	Leu	Ala	Asp		
177				485				490			495							
179	gtc	acc	gtg	aac	aag	cct	cat	ggg	gtt	cgt	cca	aag	gat	gtt	gca	gca		1536
180	Val	Thr	Val	Asn	Lys	Pro	His	Gly	Val	Arg	Pro	Lys	Asp	Val	Ala	Ala		
181				500				505			510							
183	cca	atc	gat	aag	ctg	ccc	aac	atc	aag	gat	ctg	cca	ctg	cca	cgc	ggg		1584
184	Pro	Ile	Asp	Lys	Leu	Pro	Asn	Ile	Lys	Asp	Leu	Pro	Leu	Pro	Arg	Gly		
185				515				520			525							
187	tcc	cgt	gac	cgc	ctg	aag	cag	ctt	ggc	cca	gcc	gag	ttt	gct	cgt	gat		1632
188	Ser	Arg	Asp	Arg	Leu	Lys	Gln	Leu	Gly	Pro	Ala	Ala	Phe	Ala	Arg	Asp		
189				530				535			540							
191	ctc	cgt	gag	cag	gac	gca	ctg	gca	gtt	act	gat	acc	acc	ttc	cgc	gat		1680
192	Leu	Arg	Glu	Gln	Asp	Ala	Leu	Ala	Val	Thr	Asp	Thr	Thr	Phe	Arg	Asp		
193	545				550				555			560						
195	gca	cac	cag	tct	ttg	ctt	gcg	acc	cga	gtc	cgc	tca	ttc	gca	ctg	aag		1728
196	Ala	His	Gln	Ser	Leu	Leu	Ala	Thr	Arg	Val	Arg	Ser	Phe	Ala	Leu	Lys		
197				565				570			575							
199	cct	gcg	gca	gag	gcc	gtc	gca	aag	ctg	act	cct	gag	ctt	ttg	tcc	gtg		1776
200	Pro	Ala	Ala	Glu	Ala	Val	Ala	Lys	Leu	Thr	Pro	Glu	Leu	Leu	Ser	Val		
201				580				585			590							
203	gag	gcc	tgg	ggc	ggc	gcf	acc	tac	gat	gtg	gcf	atg	cgt	ttc	ctc	ttt		1824
204	Glu	Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	Val	Ala	Met	Arg	Phe	Leu	Phe		
205				595				600			605							
207	gag	gat	ccg	tgg	gac	agg	ctc	gac	gag	ctg	cgc	gag	gcf	atg	ccg	aat		1872
208	Glu	Asp	Pro	Trp	Asp	Arg	Leu	Asp	Glu	Leu	Arg	Glu	Ala	Met	Pro	Asn		
209				610				615			620							
211	gta	aac	att	cag	atg	ctg	ttt	cgc	ggc	cgc	aac	acc	gtg	gga	tac	acc		1920
212	Val	Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	Arg	Asn	Thr	Val	Gly	Tyr	Thr		
213	625				630				635			640						
215	ccg	tac	cca	gac	tcc	gtc	tgc	cgc	gcf	ttt	gta	aag	gaa	gct	gcc	agc		1968
216	Pro	Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	Phe	Val	Lys	Glu	Ala	Ala	Ser		
217				645				650			655							
219	tcc	ggc	gtg	gac	atc	ttc	cgc	atc	ttc	gac	gca	ctt	aac	gac	gtc	tcc		2016

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220 Ser Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser		
221 660 665 670		
223 cag atg cgt cca gca atc gac gca gtc ctg gag acc aac acc gcg gta	2064	
224 Gln Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val		
225 675 680 685		
227 gcc gag gtg gct atg gct tat tct ggt gat ctc tct gat cca aat gaa	2112	
228 Ala Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu		
229 690 695 700		
231 aag ctc tac acc ctg gat tac tac cta aag atg gca gag gag atc gtc	2160	
232 Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val		
233 705 710 715 720		
235 aag tct ggc gct cac att ctg gcc att aag gat atg gct ggt ctg ctt	2208	
236 Lys Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu		
237 725 730 735		
239 cgc cca gct gcg gta acc aag ctg gtc acc gca ctg cgc cgt gaa ttc	2256	
240 Arg Pro Ala Ala Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe		
241 740 745 750		
243 gat ctg cca gtg cac gtg cac acc cac gac act gcg ggt ggc cag ttg	2304	
244 Asp Leu Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu		
245 755 760 765		
247 gct acc tac ttt gct gca gct caa gct ggt gca gat gct gtt gac ggt	2352	
248 Ala Thr Tyr Phe Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly		
249 770 775 780		
251 gct tcc gca cca ctg tct ggc acc acc tcc cag cca tcc ctg tct gcc	2400	
252 Ala Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala		
253 785 790 795 800		
255 att gtt gct gca ttc gcg cac acc cgt cgc gat acc ggt ttg agc ctc	2448	
256 Ile Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu		
257 805 810 815		
259 gag gct tct gac ctc gag ccg tac tgg gaa gct gtg cgc gga ctg	2496	
260 Glu Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu		
261 820 825 830		
263 tac ctg cca ttt gag tct gga acc cca ggc cca acc ggt cgc gtc tac	2544	
264 Tyr Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr		
265 835 840 845		
267 cgc cac gaa atc cca ggc gga cag ttg tcc aac ctg cgt gca cag gcc	2592	
268 Arg His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala		
269 850 855 860		
271 acc gca ctg ggc ctt gct gat cgc ttc gag ctc atc gaa gac aac tac	2640	
272 Thr Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr		
273 865 870 875 880		
275 gca gcc gtt aat gag atg ctg gga cgc cca acc aag gtc acc cca tcc	2688	
276 Ala Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser		
277 885 890 895		
279 tcc aag gtt gtt ggc gac ctc gca ctc cac ctg gtt ggt gcg ggt gta	2736	
280 Ser Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val		
281 900 905 910		
283 gat cca gca gac ttt gct gca gac cca caa aag tac gac atc cca gac	2784	
284 Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp		

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285	915	920	925	
287	tct gtc atc gcg ttc ctg cgc ggc gag ctt ggt aac cct cca ggt ggc			2832
288	Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly			
289	930	935	940	
291	tgg cca gaa cca ctg cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc			2880
292	Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly			
293	945	950	955	960
295	aag gca cct ctg acg gaa gtt cct gag gaa gag cag gcg cac ctc gac			2928
296	Lys Ala Pro Leu Thr Glu Val Pro Glu Glu Gln Ala His Leu Asp			
297	965	970	975	
299	gct gat gat tcc aag gaa cgt cgc aac agc ctc aac cgc ctg ctg ttc			2976
300	Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe			
301	980	985	990	
303	ccg aag cca acc gaa gag ttc ctc gag cac cgt cgc cgc ttc ggc aac			3024
304	Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Phe Gly Asn			
305	995	1000	1005	
307	acc tct gcg ctg gat gat cgt gaa ttc ttc tac gga ctg gtc gag			3069
308	Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu			
309	1010	1015	1020	
311	ggc cgc gag act ttg atc cgc ctg cca gat gtg cgc acc cca ctg			3114
312	Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu			
313	1025	1030	1035	
315	ctt gtt cgc ctg gat gcg atc tct gag cca gac gat aag ggt atg			3159
316	Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp Lys Gly Met			
317	1040	1045	1050	
319	cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca atg cgt			3204
320	Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro Met Arg			
321	1055	1060	1065	
323	gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa aag			3249
324	Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys			
325	1070	1075	1080	
327	gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt			3294
328	Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly			
329	1085	1090	1095	
331	gtt gtc act gtg act gtt gct gaa ggt gat gag gtc aag gct gga			3339
332	Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly			
333	1100	1105	1110	
335	gat gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc			3384
336	Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile			
337	1115	1120	1125	
339	act gct tct gtt gac ggc aag att gaa cgc gtt gtg gtt cct gct			3429
340	Thr Ala Ser Val Asp Gly Lys Ile Glu Arg Val Val Val Pro Ala			
341	1130	1135	1140	
343	gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taa			3474
344	Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser			
345	1145	1150	1155	
348	<210> SEQ ID NO: 2			
350	<211> LENGTH: 1157			
352	<212> TYPE: PRT			

VERIFICATION SUMMARY

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L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date